

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 28, 2003, 13:48:10 ; Search time 44 seconds
(without alignments)

2795.235 Million cell updates/sec

Title: US-09-497-822c-19

Perfect score: 4912

Sequence: 1 MEVQLGLGRVPRPSKTYR.....SVQPKILSGKVKPIYFHTQ 923

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A_Geneseq_101002:*

- 1: /SID52/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
- 2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
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- 19: /SID52/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
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- 21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4880	99.3	919	18	AAW14783
2	4880	99.3	919	21	AAW78914
3	4880	99.3	919	23	AAE19061
4	4872	99.2	919	10	AAFP93109
5	4838.5	98.5	918	20	AAV33491
6	4827.5	98.3	918	12	AAV12223
7	4814	98.0	919	10	AAFP90996
8	4201.5	85.5	902	10	AAFP10006
9	4200.5	85.5	902	10	AAFP93110
10	4187.5	85.3	902	12	AAV12224

11	2429	49.5	452	20	AAV21627	Ligand binding dom
12	2401	48.9	839	23	AAG68238	Fused androgen rec
13	2029.5	41.3	388	23	ABB83821	Human androgen rec
14	1493.5	30.4	294	23	ABB83822	Human androgen rec
15	1459	29.7	630	12	AAV12230	trpE/androgen rece
16	1349.5	27.5	260	22	AAV97073	rat androgen recep
17	1337.5	27.2	576	12	AAV12229	trpE/androgen rece
18	1261	25.7	933	20	AAV21621	Ligand binding dom
19	1256	25.6	933	21	AAV97237	Human progesterone
20	1243	25.3	246	23	AAU75930	Androgen receptor
21	1212.5	24.7	250	22	AAV55959	Human androgen rec
22	1071.5	21.8	984	20	AAV21622	Ligand binding dom
23	1069.5	21.8	984	9	AAV80922	Sequence of the hu
24	1066	21.7	1070	18	AAV17789	Green fluorescent
25	1042	21.2	777	9	AAV80919	Sequence of the pr
26	1042	21.2	777	20	AAV21623	Ligand binding dom
27	1039	21.2	777	18	AAV44700	Mutant nuclear glu
28	838	17.1	158	21	AAV78913	Androgen independe
29	795	16.2	154	20	AAV33504	Human unliganded a
30	765	15.6	251	21	AAV26786	Human progesterone
31	765	15.6	255	22	AAV97074	Rat progesterone r
32	735	15.0	630	23	ABB80766	Truncated GAL4 DBD
33	734	14.9	630	23	ABB80765	Geneswitch regulat
34	728	14.8	240	23	AAE17863	Chain A of structu
35	719	14.6	654	23	ABB80764	Geneswitch regulat
36	675.5	13.8	667	18	AAW44701	Chimeric Cre-LDB-G
37	671.5	13.7	613	22	AAE47153	Chain A of structu
38	666	13.6	215	23	AAE17861	Glucocorticoid rec
39	657.5	13.4	251	21	AAV26787	Glucocorticoid rec
40	644.5	13.1	534	17	AAV03197	A rat glucocortico
41	644	13.1	284	21	AAV19249	Glucocorticoid rec
42	636	12.9	284	19	AAW45514	Glucocorticoid rec
43	636	12.9	284	21	AAV39140	Rat glucocorticoid
44	636	12.9	284	19	AAV67559	Rat glucocorticoid
45	636	12.9	284	21	AAV78888	Glucocorticoid rec

ALIGNMENTS

RESULT 1

AAW14783
ID AAW14783 standard; Protein; 919 AA.

AC AAW14783;

AC AC

DT 22-JUN-1997 (first entry)

XX AC AAW14783;

XX AC

XX AC

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XX AC

XX AC

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XX PS Disclosure; Page 22-28; 51pp; English.

CC CC Human androgen receptor (AA14783) binds testosterone and, acting at the transcriptional level, regulates the growth of normal prostatic cells. Antisense oligonucleotides (see also AAT63200, AAT63404-05) based on an androgen receptor cDNA clone (see also AAT63407) can be used to prevent androgen receptor gene expression, thereby inhibiting the growth or survival of prostatic cells for the treatment of benign prostatic hyperplasia and prostate cancer.

XX SQ Sequence 919 AA;

Query Match 99.3%; Score 4880; DB 18; Length 919;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 919; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy 1 MEVOLGLGRVYPPPSKTYRGAFQNLFSQVREVIONFGRHPEAASAPPGASLLLOQQ 60
Db 1 MEVOLGLGRVYPPPSKTYRGAFQNLFSQVREVIONFGRHPEAASAPPGASLLLL--- 57

Qy 61 QQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 120
Db 58 -QQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 116

Qy 121 POSALECHPERGCVPEPNAASKGLPQPLPAPDEDDSAAPSTLSLGLPTFPGLSGCS 180
Db 117 POSALECHPERGCVPEPNAASKGLPQPLPAPDEDDSAAPSTLSLGLPTFPGLSGCS 176

Qy 181 ADLKDILSEASTMQLLOQQQQQAVSESSSGRAREASGAPTSSKDNLYLGGTSTISDNAKE 240
Db 177 ADLKDILSEASTMQLLOQQQQQAVSESSSGRAREASGAPTSSKDNLYLGGTSTISDNAKE 236

Qy 241 LCAVSVSMGLGVEALEHLSPEQLRGDCMYAPLLGVPVAVRTPCAPLAECKSILLDD 300
Db 237 LCAVSVSMGLGVEALEHLSPEQLRGDCMYAPLLGVPVAVRTPCAPLAECKSILLDD 296

Qy 301 AGKSTEDTAYSPFKGGYTKLEGESLGCSSAAGSSGTLELPSTLSLYKSGALDEAAA 360
Db 297 AGKSTEDTAYSPFKGGYTKLEGESLGCSSAAGSSGTLELPSTLSLYKSGALDEAAA 356

Qy 361 YQSRDYNNFLALAGPPPPPPHPPHARIKLENPLDYGSAAAAAQQCRGYDLASLHGAG 420
Db 357 YQSRDYNNFLALAGPPPPPPHPPHARIKLENPLDYGSAAAAAQQCRGYDLASLHGAG 416

Qy 421 AAGPGSGPSAAASSWHTLFTABEGQLYPCGGGGGGGGGGGGGGGGGGGGGGEAGA 480
Db 417 AAGPGSGPSAAASSWHTLFTABEGQLYPCGGGGGGGGGGGGGGGGGGGGGGEAGA 476

Qy 481 VAPGYTRPPQLAGQESDFTAPDWWPGMVSRVPPSPCTCVKSEMGPMWDSYSGPYGD 540
Db 477 VAPGYTRPPQLAGQESDFTAPDWWPGMVSRVPPSPCTCVKSEMGPMWDSYSGPYGD 536

Qy 541 MRLETARDHVLPIIDYFFPQKTLICGDEASGCHYGALTGCGCKVFFKRAEKGKYLCA 600
Db 537 MRLETARDHVLPIIDYFFPQKTLICGDEASGCHYGALTGCGCKVFFKRAEKGKYLCA 596

Qy 601 SRNDCTIDFRKNCPSRLKRCYKAGTGLGARKLKLGNLKLQECASSTTSPTETTT 660
Db 597 SRNDCTIDFRKNCPSRLKRCYKAGTGLGARKLKLGNLKLQECASSTTSPTETTT 656

Qy 661 QKTVSHIEGECQPIFNVLNLEAIPGVYVAGHNNOPDSFAALLSSNLGEROLVHV 720
Db 657 QKTVSHIEGECQPIFNVLNLEAIPGVYVAGHNNOPDSFAALLSSNLGEROLVHV 716

Qy 721 KWAKALPGFNLHVDQMAVIOYSWGLMVFAMGWSFTNVNSRMLYFAPDLVFNRYRMH 780
Db 717 KWAKALPGFNLHVDQMAVIOYSWGLMVFAMGWSFTNVNSRMLYFAPDLVFNRYRMH 776

Qy 781 KSRMYSCQVRMHLSEQECNLQITPOEFLCNKALLIESIIPVDGLKNQKFFDELMMYIK 840
Db 777 KSRMYSCQVRMHLSEQECNLQITPOEFLCNKALLIESIIPVDGLKNQKFFDELMMYIK 836

Qy 841 ELDRIIACKKNPTSCSRREYQLTLLKDSVQPIARELHQFTDILLIKSHMVSVDPEKMA 900
Db 837 ELDRIIACKKNPTSCSRREYQLTLLKDSVQPIARELHQFTDILLIKSHMVSVDPEKMA 896

Qy 901 EIISVQVQPKILSGKVKPIYPHTQ 923
Db 897 EIISVQVQPKILSGKVKPIYPHTQ 919

RESULT 2
AAV78914
ID AAV78914 standard; protein; 919 AA.
XX AC AAV78914;
XX DT 23-MAY-2000 (first entry)
XX DE Human androgen receptor (AR) amino acid sequence.
XX KW Androgen receptor; AR; androgen-independent activation; inhibitor;
XX KW cancer; benign prostatic hyperplasia; hirsutism; androgenic alopecia;
XX KW acne; breast cancer; Kennedy disease; prostate cancer.
XX OS Homo sapiens.
XX PN WO200001813-A2.
XX PD 13-JAN-2000.
XX PF 30-JUN-1999; 99WO-CA00604.
XX PR 30-JUN-1998; 98US-0091871.
XX PA (UYBR-) UNIV BRITISH COLUMBIA.
XX PI Sadar MD, Bruchovsky N, Gout PW, Snoek R, Mawji NR;
XX DR WPI; 2000-182113/16.
XX PT Novel non-androgen ligand binding peptides for inhibiting
PT androgen-independent activation of androgen receptor, used for
PT screening compounds and for treatment of androgen-mediated diseases.
PT such as prostate cancer
XX PS Disclosure; Page 7; 32pp; English.
XX CC This sequence represents the human androgen receptor (AR) amino acid
CC sequence. The invention relates to a fragment of the AR corresponding to
CC amino acids 234-391 (see AAV78913). The fragment mediates
CC androgen-independent activation of the AR. The androgen receptor acts as
CC a transcription factor, regulating the expression of certain
CC androgen-responsive genes. Interaction of the AR with the protein kinase
CC A signal transduction pathway involves interaction with the androgen
CC independent region. The AR fragment and peptides derived from it can be
CC used as agents for inhibiting androgen independent activation of the
CC androgen receptor, as activation domains, and as a tool for screening
CC for compounds which affect androgen-independent activation of the AR.
CC The peptides, when used in combination with androgen deprivation,
CC effectively limit androgen mediated disease progression. These diseases
CC include cancer, benign prostatic hyperplasia, hirsutism, androgenic
CC alopecia, acne, breast cancer, Kennedy disease, and especially prostate
CC cancer. The peptides and nucleic acids encoding them, are especially used
CC for the treatment of androgen-mediated diseases, especially prostate
CC tumours in patients deprived of androgen.
XX SQ Sequence 919 AA;

Query Match 99.3%; Score 4880; DB 21; Length 919;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 919; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy 1 MEVOLGLGRVYPPPSKTYRGAFQNLFSQVREVIONFGRHPEAASAPPGASLLLOQQ 60
Db 1 MEVOLGLGRVYPPPSKTYRGAFQNLFSQVREVIONFGRHPEAASAPPGASLLLOQQ 60

Db 1 MEVQLGLGRVYPRPPSKTYRGAFQNLFGSVREVIONGPRHPEAASAPPGASLLLL--- 57
 QY 61 QQQQQQQQQQQQQQQQQQQQQQQQQQQETSPROQQQQQGGEDGSPQAHRRGPTGYLVLDDEEQPSQ 120
 Db 58 -QQQQQQQQQQQQQQQQQQQQQQQQQQETSPROQQQQQGGEDGSPQAHRRGPTGYLVLDDEEQPSQ 116
 QY 121 QSALECHPERGCVPEPGAAVAASKGLPQPLPAPPPDEDDSAAPSTLSLLGPTFFGLSSCS 180
 Db 117 QSALECHPERGCVPEPGAAVAASKGLPQPLPAPPPDEDDSAAPSTLSLLGPTFFGLSSCS 176
 QY 181 ADLKDILSEASTMOLLOQQQOEAVSESSSGRAREASGAPTSSKDNLYGTTISDNAME 240
 Db 177 ADLKDILSEASTMOLLOQQQOEAVSESSSGRAREASGAPTSSKDNLYGTTISDNAME 236
 QY 241 LKAVSVSMGLGVLEHLSPEQLRGDCMYAPLLGVPPAVRPTPCAPLAECGSLDDDS 300
 Db 237 LKAVSVSMGLGVLEHLSPEQLRGDCMYAPLLGVPPAVRPTPCAPLAECGSLDDDS 296
 QY 301 AGKSTEDTAESYSPFKGGYTKLGESLGCSSGSAAGSGTLELPSTLSLYKSGALDEAAA 360
 Db 297 AGKSTEDTAESYSPFKGGYTKLGESLGCSSGSAAGSGTLELPSTLSLYKSGALDEAAA 356
 QY 361 YQSRDYNFPLALAGPPPPPPHARIKLENPLDYGSAAAAAOCRYGDLASLHGAG 420
 Db 357 YQSRDYNFPLALAGPPPPPPHARIKLENPLDYGSAAAAAOCRYGDLASLHGAG 416
 QY 421 AAGPGSGSPSAAASSSWHTLFTAEGLYGCPCGGGGGGGGGGGGGGGGGGGGEAGA 480
 Db 417 AAGPGSGSPSAAASSSWHTLFTAEGLYGCPCGGGGGGGGGGGGGGGGGGGGEAGA 476
 QY 481 VAPGYTRPQGLAGQSDFTADVWYPGGWSRVYPPSPCTCVKSEMGPMDSYSGPYGD 540
 Db 477 VAPGYTRPQGLAGQSDFTADVWYPGGWSRVYPPSPCTCVKSEMGPMDSYSGPYGD 536
 QY 541 MRLETARDHVLPIIDYFPPOKTLICGDEASGCHYGALTCGCKVFFKRAAEKQKYLCA 600
 Db 537 MRLETARDHVLPIIDYFPPOKTLICGDEASGCHYGALTCGCKVFFKRAAEKQKYLCA 596
 QY 601 SRNDCTIDKFRKNCPSCLRKCYEAGMTLGARKLKLNLKLOEAGEASSTTSPEETT 660
 Db 597 SRNDCTIDKFRKNCPSCLRKCYEAGMTLGARKLKLNLKLOEAGEASSTTSPEETT 656
 QY 661 QKLTVSHIEGYEQPIFLNVLEAIEPGVVCAGHDNNQDPSFALLSSLNELGERQLVHVY 720
 Db 657 QKLTVSHIEGYEQPIFLNVLEAIEPGVVCAGHDNNQDPSFALLSSLNELGERQLVHVY 716
 QY 721 KWAKALPGFRNLHVDDQMAVIOYSWMGLMVFAMGWRSTNVNSRMLYFAPDLVFNERYMH 780
 Db 717 KWAKALPGFRNLHVDDQMAVIOYSWMGLMVFAMGWRSTNVNSRMLYFAPDLVFNERYMH 776
 QY 781 KSRMYSQVVRMHLSDQFGLWLTPOEFLCMKALLLSIIPVDGLKNOKFFDELRMNYIK 840
 Db 777 KSRMYSQVVRMHLSDQFGLWLTPOEFLCMKALLLSIIPVDGLKNOKFFDELRMNYIK 836
 QY 841 ELDRITACKKNPTSCSRFYOLTLLKDSVQPIARELHOFTDILLIKSHWVSDFPEMMA 900
 Db 837 ELDRITACKKNPTSCSRFYOLTLLKDSVQPIARELHOFTDILLIKSHWVSDFPEMMA 896
 QY 901 EILISVQPKILSGKVKPIYFHTQ 923
 Db 897 EILISVQPKILSGKVKPIYFHTQ 919
 RESULT 3
 ID AAE19061
 XX AAE19061 standard; Protein; 919 AA.
 AC AAE19061;
 XX
 DT 21-MAY-2002 (first entry)
 XX Human androgen receptor (AR).
 DE
 XX

KW Human; AIB1; amplified in breast cancer 1; androgen receptor; AR;
 KW prostate cancer; chromosome X.
 OS Homo sapiens.
 XX WO200210452-A2.
 XX 07-FEB-2002.
 XX 27-JUL-2001; 2001WO-US23834.
 XX 27-JUL-2000; 2000US-221074P.
 PA (UYRP) UNIV ROCHESTER.
 XX Chang C;
 XX WPI; 2002-206195/26.
 XX N-PSDB; AND30440.
 PT Assessing the risk of acquiring or developing prostate cancer in a
 PT human subject, comprises determining the length of the contiguous CAG,
 PT CAA and/or GGN repeats in the AIB1 gene and/or androgen receptor gene
 PT of the subject.
 XX
 PS Disclosure; Page 62-63; 86pp; English.
 CC The invention relates to a method for assessing the risk of prostate
 CC cancer in a human subject. The method involves determining the length
 CC of the contiguous CAG or CAA repeats in both AIB1 (Amplified In Breast
 CC cancer 1) gene alleles or contiguous CAG, CAA or GGN repeats in the
 CC androgen receptor gene of the subject. The method is useful for
 CC assessing a subject's risk for acquiring or developing prostate cancer.
 CC The present sequence is human androgen receptor (AR) protein. Human
 CC AR gene is located on X chromosome.
 XX
 SQ Sequence 919 AA;
 Query Match 99.3%; Score 4880; DB 23; Length 919;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 919; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
 QY 1 MEVQLGLGRVYPRPPSKTYRGAFQNLFGSVREVIONGPRHPEAASAPPGASLLLLQQQ 60
 Db 1 MEVQLGLGRVYPRPPSKTYRGAFQNLFGSVREVIONGPRHPEAASAPPGASLLLL--- 57
 QY 61 QQQQQQQQQQQQQQQQQQQQQQQQQQQETSPROQQQQQGGEDGSPQAHRRGPTGYLVLDDEEQPSQ 120
 Db 58 -QQQQQQQQQQQQQQQQQQQQQQQQQQETSPROQQQQQGGEDGSPQAHRRGPTGYLVLDDEEQPSQ 116
 QY 121 QSALECHPERGCVPEPGAAVAASKGLPQPLPAPPPDEDDSAAPSTLSLLGPTFFGLSSCS 180
 Db 117 QSALECHPERGCVPEPGAAVAASKGLPQPLPAPPPDEDDSAAPSTLSLLGPTFFGLSSCS 176
 QY 181 ADLKDILSEASTMOLLOQQQOEAVSESSSGRAREASGAPTSSKDNLYGTTISDNAME 240
 Db 177 ADLKDILSEASTMOLLOQQQOEAVSESSSGRAREASGAPTSSKDNLYGTTISDNAME 236
 QY 241 LKAVSVSMGLGVLEHLSPEQLRGDCMYAPLLGVPPAVRPTPCAPLAECGSLDDDS 300
 Db 237 LKAVSVSMGLGVLEHLSPEQLRGDCMYAPLLGVPPAVRPTPCAPLAECGSLDDDS 296
 QY 301 AGKSTEDTAESYSPFKGGYTKLGESLGCSSGSAAGSGTLELPSTLSLYKSGALDEAAA 360
 Db 297 AGKSTEDTAESYSPFKGGYTKLGESLGCSSGSAAGSGTLELPSTLSLYKSGALDEAAA 356
 QY 361 YQSRDYNFPLALAGPPPPPPHARIKLENPLDYGSAAAAAOCRYGDLASLHGAG 420
 Db 357 YQSRDYNFPLALAGPPPPPPHARIKLENPLDYGSAAAAAOCRYGDLASLHGAG 416
 QY 421 AAGPGSGSPSAAASSSWHTLFTAEGLYGCPCGGGGGGGGGGGGGGGGGGGGEAGA 480
 Db 417 AAGPGSGSPSAAASSSWHTLFTAEGLYGCPCGGGGGGGGGGGGGGGGGGGGEAGA 476

CC prostate cancers to determine responsiveness to androgen withdrawal
CC therapy.

XX
SO Sequence 919 AA;

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Query Match          99.2%; Score 4872; DB 10; Length 919;
Best Local Similarity 99.5%; Pred. NO. 0;
Matches 918; Conservative 0; Mismatches 1; Indels 4

```

481	QY	VAPYGYTRPQGLAGQESDFTAPDWWYVPGGVMVSRVPYSPCTCVKSEMGPMWMDSYSGPYGD	540
477	Db	VAPYGYTRPQGLAGQESDFTAPDWWYVPGGVMVSRVPYSPCTCVKSEMGPMWMDSYSGPYGD	536
541	QY	MRLETPARDHVLPIIDYFFPQKTCLLCGDBASCHYGALTGCSCKVFFRRAAEGKQKYLCA	600
537	Db	MRLETPARDHVLPIIDYFFPQKTCLLCGDBASCHYGALTGCSCKVFFRRAAEGKQKYLCA	596
601	QY	SRNDCTIDAFRRKNPCSCRRLKCYEAGMTLGARKLKLGNLKLQEBEGEASSTTSPTEETT	660
597	Db	SRNDCTIDAFRRKNPCSCRRLKCYEAGMTLGARKLKLGNLKLQEBEGEASSTTSPTEETT	656
661	QY	QKLTVSHIEGYEQOPIFLNVLPAIBPGVVCAGHDNNQDPSFAALLSSLNELLGEROLVHVW	720
657	Db	QKLTVSHIEGYEQOPIFLNVLPAIBPGVVCAGHDNNQDPSFAALLSSLNELLGEROLVHVW	716
721	QY	KWAKALPGFNLHVDQMAVIOYSWMGLVMFAMGWRSTNVNSRMLYFAPDLVFNEXYRMH	780
717	Db	KWAKALPGFNLHVDQMAVIOYSWMGLVMFAMGWRSTNVNSRMLYFAPDLVFNEXYRMH	776
781	QY	KSRMYSQCVNRMRHLSQEFQWLIQTPOEFTCMKALLFSIIPVDGLKNQKFFDELRMNYIK	840
777	Db	KSRMYSQCVNRMRHLSQEFQWLIQTPOEFTCMKALLFSIIPVDGLKNQKFFDELRMNYIK	836
841	QY	ELDRITIAACKRNKNTSCSRRFYQLTLLKDSVQPIARELHQFTFDLTIKSHMWSVDFPEMMA	900
837	Db	ELDRITIAACKRNKNTSCSRRFYQLTLLKDSVQPIARELHQFTFDLTIKSHMWSVDFPEMMA	896
901	QY	EIISVQVPKILSGKVRPYFHTQ	923
897	Db	EIISVQVPKILSGKVRPYFHTQ	919

RESULT 4

RESULTS &
AAP93109
ID AAP93109 standard: protein: 919 AA.

ID
yy
AAFP93109

XX
3303100.AC
AAP93109;XX
DE
19-MAR-1990 (first entry)

DT 19-MAR-19

XX Human androgen receptor

DE Human and

[illegible]

KW Human and

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OS Homo sapi

XX

PN WO8909791

XX XX

PD 19-OCT-19

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PF 13-APR-19

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PR 14-APR-19

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PA (UYNC-) U

XX

PI French FS

XX

DR WPI; 1989-324206/

DR N-PSDB; AAN91772.

XX

PT DNA encoding androgen receptor protein - useful for transforming

PT eukaryotic hosts for protein expression and subsequent antibody production.

XX

PS Disclosure

XX

CC Androgen

antibodies. These are used for the detection and quantification of AR in the presence of endogenous androgen, as androgen will not interfere with binding. They may be used in assays to determine and quantify cellular distribution of AR in tumour tissue, and are esp. useful for evaluating

RESULT 5

AAAY33491
ID AAAY33491 standard; Protein; 918 AA.

AC AAY33491;

DT 19-JAN-2000 (first entry)

DE Human androgen receptor protein.

KW Proapoptotic; dependence domain; p75NTR; androgen receptor; DCC;
 KW huntingtin polypeptide; Machado-Joseph disease; SCAl; SCAl; SCAl;
 KW atrophin-1; cell death; apoptosis; Huntington's disease; head trauma;
 KW Alzheimer's disease; Kennedy's disease; spinocerebellar ataxia; stroke;
 KW dentatorubral pallidoluysian atrophy; cell proliferation; cell survival;
 KW neoplastic; malignant; autoimmune; fibrotic.

OS Homo sapiens.

PN WO9945944-A1.

16-SEP-1999

11-MAR-1999:

12-MAR-1998.

XX
PA : (BITRN-) BITRNL

XX
PT
Bredeson DE

XX
OR
WDT: 1000-561

DR N-PSDB; AAZ23

New proapopto

3
2
1

XX
XX

which comprises

huntingtin po

of inducing c

a proapoptotic

Spino cerebelli.

reducing the
MacLadd-Josep

cell prolifer:
autoimmune or

androgen receptor

sequence 914

Query Match
Best Local Similarity

Matches 914; Cc

Y 1 MEVQLGLG

b1 MEVQLGLGFI

61 QQQQQQQQQQ

b ----- 58

121 PQSALECHH

113 PQSALECHF

PN WO9107423-A.
XX 30-MAY-1991.
XX 19-OCT-1990; 90WO-US06015.
XX 17-NOV-1989; 89US-0438775.
XX (ARCH-) ARCH DEV CORP.
XX Liao S, Chang C;
XX WPI; 1991-178048/24.
XX N-PSDB; AAQ12001.
XX Androgen receptor and TR2 DNA binding proteins - DNA sequences
XX and antibodies for detection and quantification methods
XX Claim 25; Fig 3; 79pp; English.
XX This sequence was deduced from a cDNA clone isolated by screening
XX commercially available human testis and prostate lambda gtl1 cDNA
XX libraries. The sequence is very similar to that of rat AR and in
XX the DNA-binding domain it is identical to that of rAR DNA-binding
XX domain. Homology comparisons with other known steroid receptors
XX indicate that hAR is more closely related to glucocorticoid,
XX mineralo-corticoid and progesterone receptors than to v-erb-A or to
XX receptors for oestrogen, vitamin D and thyroid hormones.
XX Sequence 918 AA:
SQ
Query Match 98.38; Score 4827.5; DB 12; Length 918;
Best Local Similarity 98.58; Pred. No. 4.2e-317;
Matches 912; Conservative 1; Mismatches 2; Indels 11; Gaps 2;
QY 1 MEVQLGLGRVYPRPSTYRTYRGAFQNLQSVREVIVQNPGRHPHAAAPPGASLLILQQO 60
DB 1 MEVQLGLGRVYPRPSTYRTYRGAFQNLQSVREVIVQNPGRHPHAAAPPGASLLIL --- 57
QY 61 QQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 120
DB 58 -----QQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 112
QY 121 PQSALECHPERGCVPEPGEAAVAASKGLPQQLPAPPDEDDSAAPSTLSLLGPTFPGLSSCS 180
DB 113 PQSALECHPERGCVPEPGEAAVAASKGLPQQLPAPPDEDDSAAPSTLSLLGPTFPGLSSCS 172
QY 181 ADLKILSPASTMQLQQQQQQQEAIVSEGSRRAREASCAPTSSKDNVLTGTTSTISDNKE 240
DB 173 ADLKILSPASTMQLQQQQQQQEAIVSEGSRRAREASCAPTSSKDNVLTGTTSTISDNKE 232
QY 241 LCKAVSVSMGLGVEALEHLSPEQLRGDCMYAPLLGVPPAVRPTPCAPLAECKGSLDDDS 300
DB 233 LCKAVSVSMGLGVEALEHLSPEQLRGDCMYAPLLGVPPAVRPTPCAPLAECKGSLDDDS 292
QY 301 AGKSTEDTAESYSPFGKGYTKLGESLGCSSAAAGSGTLELSTLSLYKSGALDEAAA 360
DB 293 AGKSTEDTAESYSPFGKGYTKLGESLGCSSAAAGSGTLELSTLSLYKSGALDEAAA 352
QY 361 YQSRDYNNFLALAGPPPPPPPPHARIKLENPLDYGSAWAAAAAACRYGDLASLHGAG 420
DB 353 YQSRDYNNFLALAGPPPPPPPPHARIKLENPLDYGSAWAAAAAACRYGDLASLHGAG 412
QY 421 AAGFGSGSPSAAASSWHLTFTAEQGQLYGPC---GGGGGGGGGGGGGGGGGGGGGGGG 477
DB 413 AARPGSGSPSAAASSWHLTFTAEQGQLYGPCGGGGGGGGGGGGGGGGGGGGGGGGGG 472
QY 478 AGAVAPYGYRTRPQGLAGQESDFTAPDVMYPCGMVSRYPSPCTCKSEMGPWMDYSYSGP 537
DB 473 AEAVAPYGYRTRPQGLAGQESDFTAPDVMYPCGMVSRYPSPCTCKSEMGPWMDYSYSGP 532
QY 538 YGDMRLTARDHVLPIDYFFPPQKTLICGDEASGCHYGALTGCKVCKFFRAAEGKQY 597
|||||

DB 533 YGDMRLTARDHVLPIDYFFPPQKTLICGDEASGCHYGALTGCKVCKFFRAAEGKQY 592
QY 598 LCASRNDCTIDKFRKNCPSCLRKCYEAGMTLGARKLKLGNLKLQEEGEASSTTSPT 657
DB 593 LCASRNDCTIDKFRKNCPSCLRKCYEAGMTLGARKLKLGNLKLQEEGEASSTTSPT 652
QY 658 ETTQKLTVSHIEGYECQPIFLNLVLEAIEPVGVCAGHDNNQPDFAALLSSINELGERQLV 717
DB 653 ETTQKLTVSHIEGYECQPIFLNLVLEAIEPVGVCAGHDNNQPDFAALLSSINELGERQLV 712
QY 718 HVYKAKALPGFRNLHVDQMAVIOYSWMLMVFAMGWRSTNNVNSRMLYFAPDLVFNEX 777
DB 713 HVYKAKALPGFRNLHVDQMAVIOYSWMLMVFAMGWRSTNNVNSRMLYFAPDLVFNEX 772
QY 778 RMHKSRYMOCVSRMHLQSFQGLQITPQEFCLMKALLFSIIPVDGLKNOKFFDELRLMN 837
DB 773 RMHKSRYMOCVSRMHLQSFQGLQITPQEFCLMKALLFSIIPVDGLKNOKFFDELRLMN 832
QY 838 YIKELDRITACRKNPTSCRRPYQLTKLLDSVQPIARELHQFTFDLLIKSHMVSVDPE 897
DB 833 YIKELDRITACRKNPTSCRRPYQLTKLLDSVQPIARELHQFTFDLLIKSHMVSVDPE 892
QY 898 MMAEILSVQVPKILSGKVKPIVFHTQ 923
DB 893 MMAEILSVQVPKILSGKVKPIVFHTQ 918
RESULT 7
AAP90996
ID AAP90996 standard; protein; 919 AA.
XX AAP90996;
XX 28-FEB-1990 (first entry)
XX Human androgen receptor DNA clone.
XX Androgen receptor; TR2 polypeptide;
XX Homo sapiens.
XX Key Location/Qualifiers
FH Region 1..919
FT /*tag= a
FT /product=98 kD polypeptide
FT 185..919
FT /*tag= b
FT /product=79 kD polypeptide
XX WO8909223-A.
XX 05-OCT-1989.
XX 24-MAR-1989; 89WO-US01238.
XX 30-MAR-1988; 88US-0176107.
XX (ARCH-) ARCH DEVELOPMENT CORP.
XX Liao S, Chang C;
XX WPI; 1989-309501/42.
XX N-PSDB; AAN91577.
XX New DNA encoding new androgen receptor and TR2 polypeptide(s) - able
XX to bind DNA, and derived antibodies, useful for receptor assay and
XX purification.
XX Claim 8; Fig 3; 60pp; English.
XX The protein is used to raise antibodies for receptor assays and for
XX affinity purification.
XX The 98 kD product starts at the first Met codon; the 79 kD product
CC

CC starts from the second.

XX Sequence 919 AA;

```
Query Match      98.0%; Score 4814; DB 10; Length 919;
Best Local Similarity 98.4%; Pred. No. 3.5e-316;
Matches 912; Conservative 0; Mismatches 3; Indels 12; Gaps 3;

QY 1 MEVQLGLGRVYPRPSTKYRGAFONLFQSVREVIONPGPRHPEAASAAPGASLLLLQQQ 60
Db 1 MEVQLGLGRVYPRPSTKYRGAFONLFQSVREVIONPGPRHPEAASAAPGASLLLL--- 57
QY 61 QQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ- GEDGSPQAHRRGPTGYLVLDDEEQPS 119
Db 58 -----QQQQQQQQQQQQQQQQQQQQQQQQQQQQQSTPTQQQQQQHGEDGSPQAHRRGPTGYLVLDDEEQPS 112
QY 120 QPSALECHPERGCVPEPGAASAKGLPQPLPAPDEDDSAAPSTLSLGGTFFGLSSC 179
Db 113 QPSALECHPERGCVPEPGAASAKGLPQPLPAPDEDDSAAPSTLSLGGTFFGLSSC 172
QY 180 SADLKDILSEASTWQLLQQQQQAVSEGSSGRAREASGAPTSSKDNVILGTTSTISDNK 239
Db 173 SADLKDILSEASTWQLLQQQQQAVSEGSSGRAREASGAPTSSKDNVILGTTSTISDNK 232
QY 240 ELCKAVSVSMGLGVEALEHLSPEQQLRGDCMVAPILGYPPAVRPTPCAPLAECKGSLDD 299
Db 233 ELCKAVSVSMGLGVEALEHLSPEQQLRGDCMVAPILGYPPAVRPTPCAPLAECKGSLDD 292
QY 300 SAKGSTEDTAEYSPFKGGYTKLEGESLCSGSAAGSSGTTLELPSLTSLYKSGALDEAA 359
Db 293 SAKGSTEDTAEYSPFKGGYTKLEGESLCSGSAAGSSGTTLELPSLTSLYKSGALDEAA 352
QY 360 AYQSRDYNFPLALAGPPPPPPHARIKLENPLDYGSAWAAAAACRYDGLASLHGA 419
Db 353 AYQSRDYNFPLALAGPPPPPPHARIKLENPLDYGSAWAAAAACRYDGLASLHGA 412
QY 420 GAAGPGSGPSAAAASSWHTLFTABEGQLYGPC---GGGGGGGGGGGGGGGGGGGGGG 476
Db 413 GAAGPGSGPSAAAASSWHTLFTABEGQLYGPCGGGGGGGGGGGGGGGGGGGGGGGG 472
QY 477 EACAVAPYGYTRPPQGLAQESDFAPDVWYPPGMVSRVYPSPTCVKSEMPWMDSYSG 536
Db 473 EACAVAPYGYTRPPQGLAQESDFAPDVWYPPGMVSRVYPSPTCVKSEMPWMDSYSG 532
QY 537 PYGDMRLETARDHVLPIIDYFPPOKTCLICGDEASGCHYGALTCGCKVFPFKRAEKGK 596
Db 533 PYGDMRLETARDHVLPIIDYFPPOKTCLICGDEASGCHYGALTCGCKVFPFKRAEKGK 592
QY 597 YLCASRNDCTIDKFRKNCPCRLKCYEAGMTLGARKLKLGNLKLQEEGEASSTTSPT 656
Db 593 YLCASRNDCTIDKFRKNCPCRLKCYEAGMTLGARKLKLGNLKLQEEGEASSTTSPT 652
QY 657 EETTKLTVSHTEGECOPIFLNVLAEPTGVVCAHDNNQPDFAALLSSNLNGLERQL 716
Db 653 EETTKLTVSHTEGECOPIFLNVLAEPTGVVCAHDNNQPDFAALLSSNLNGLERQL 712
QY 717 VHVWKAALPGFRLHLVDQMAVITQSWMGLVMFAMGWRSTFNVNSRMLYEAPDLVFNE 776
Db 713 VHVWKAALPGFRLHLVDQMAVITQSWMGLVMFAMGWRSTFNVNSRMLYEAPDLVFNE 772
QY 777 YRMHKSRYVQCVNRHLSQEGWLQITPOEFLCMKALLFSIIPVDGLKNQKFFDELRM 836
Db 773 YRMHKSRYVQCVNRHLSQEGWLQITPOEFLCMKALLFSIIPVDGLKNQKFFDELRM 832
QY 837 NYIKELDRILIAKRNKPTSCRRRYQLTKLDSVQPTARELHFTFDLLIKSHMWSVDFP 896
Db 833 NYIKELDRILIAKRNKPTSCRRRYQLTKLDSVQPTARELHFTFDLLIKSHMWSVDFP 892
QY 897 ENMAEIIISVQPKILSGKVKPIYFHTQ 923
Db 893 ENMAEIIISVQPKILSGKVKPIYFHTQ 919
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RESULT 8
AAP91006
ID AAP91006 standard; protein; 902 AA.
XX
XX AAP91006;
XX AC
XX DT 28-FEB-1990 (first entry)
XX DE Rat androgen receptor DNA clone.
XX KW Androgen receptor; TR2 polypeptide;
XX OS Rat.
XX FH Key Location/Qualifiers
FT Region 1..902
FT FT /*tag= a
FT FT /product=98 kD polypeptide
FT FT 170..902
FT FT /*tag= b
FT FT /product=79 kD polypeptide
PN WO8909223-A.
XX
XX 05-OCT-1989.
XX
XX 24-MAR-1989; 89WO-US01238.
XX
XX 30-MAR-1988; 88US-0176107.
XX
XX (ARCH-) ARCH DEVELOPMENT CORP.
XX
XX Liao S, Chang C;
XX
XX WPI: 1989-309501/42.
XX N-PSDB; AAN91578.
XX
XX New DNA encoding new androgen receptor and TR2 polypeptide(s) - able
XX to bind DNA, and derived antibodies, useful for receptor assay and
XX purification.
XX
XX Claim 8; Fig 3; 60pp; English.
XX
XX The protein is used to raise antibodies for receptor assays and for
XX affinity purification.
XX The 98 kD product starts at the first Met codon; the 79 kD product
XX starts from the second.
XX
XX Sequence 902 AA;
XX
Query Match      85.5%; Score 4201.5; DB 10; Length 502;
Best Local Similarity 84.6%; Pred. No. 7.2e-275;
Matches 796; Conservative 36; Mismatches 52; Indels 57; Gaps 4;

QY 1 MEVQLGLGRVYPRPSTKYRGAFONLFQSVREVIONPGPRHPEAASAAPGASLLLLQQQ 60
Db 1 MEVHLGLGRVYPRPSTKYRGAFONLFQSVREVIONPGPRHPEAASIAAPGACL----- 54
QY 61 QQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ- GEDGSPQAHRRGPTGYLVLDDEEQPS 119
Db 55 -----QQQQTSPRRRRRQHPEDGSPQAHIRGTTGYLALDEEQPS 96
QY 120 QPSALECHPERGCVPEPGAASAKGLPQPLPAPDEDDSAAPSTLSLGGTFFGLSSC 179
Db 97 QQQSASEGHPESGCLPEPGAATAPGKLPQPPAPDQDDSAAPSTLSLGGTFFGLSSC 156
QY 180 SADLKDILSEASTWQLL-----QQQQQAVSEGSSGRAREASGAPTS 222
Db 157 SADLKDILSEASTWQLLQQQQQQQQQQQQQQQQQQQQQEVISEGSSSVRAREATGAPSS 216
QY 223 SKDNVILGTTSTISDNKELCKAVSVSMGLGVEALEHLSPEQQLRGDCMVAPILGYPPAVR 282
Db 217 SKDSYLGNSITSDSAKELCKAVSVSMGLGVEALEHLSPEQQLRGDCMVAPILGYPPAVR 276
```


XX OS Homo sapiens.
XX PN W09926966-A2.
XX PD 03-JUN-1999.
XX PF 25-NOV-1998; 98WO-US25296.
XX PR 26-NOV-1997; 9705-0980115.
XX PA (RBGC) UNIV CALIFORNIA.
XX PI Apriletti JW, Baxter JD, Fletterick RJ, Kushner PJ;
XX PI Scanlan TS, Shiau AK, Wagner RL, West BL;
XX WPI: 1999-357810/30.
XX PT Modulating activity of a thyroid hormone receptor
XX PS Disclosure; Fig 3H-R; 447pp; English.
XX CC The invention relates to a method for modulating activity of a thyroid
XX CC hormone receptor that comprises administration of an aromatic compound
XX CC which fits spatially and preferentially into a thyroid hormone ligand
XX CC binding domain. The aromatic compound (of a specified formula) can be
XX CC used to increase alpha-glycerophosphate dehydrogenase (GPDH) levels, at
XX CC levels which do not significantly modify cardiac GPDH levels and are
XX CC indicated in the treatment of obesity. The compound also lower total
XX CC plasma cholesterol and triglyceride levels and can be used as anti-
XX CC hypertriglyceridaemic agents. The compound may also be used for treating
XX CC atherosclerosis and may be indicated in thyroid hormone replacement
XX CC therapy in patients with compromised cardiac function. Sequences
XX CC AAY21621- 636 amino acid sequences of ligand binding domains of several
XX CC members of the nuclear receptor superfamily.
XX SQ Sequence 452 AA;
Query Match 49.5%; Score 2429; DB 20; Length 452;
Best Local Similarity 99.8%; Pred. No. 1.2e-155;
Matches 451; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 472 GGGGAGAVPYGYTRPPQGLAGQESDFTAPDVWPGMVSRVYPSPPTCKSEMGPWM 531
Db 1 GGGGAGAVPYGYTRPPQGLAGQESDFTAPDVWPGMVSRVYPSPPTCKSEMGPWM 60
QY 532 DSYSGPYGDMRLTARDHVLPIIDYFPPOKTLICGDEASGCHYGALTCGSKVFFKRAA 591
Db 61 DSYSGPYGDMRLTARDHVLPIIDYFPPOKTLICGDEASGCHYGALTCGSKVFFKRAA 120
QY 592 EGKQKYLCAASNDCTIDKFRKNCPSRLKRCYEAGMTLGARKLKLGNLKLQEEGEASS 651
Db 121 EGKQKYLCAASNDCTIDKFRKNCPSRLKRCYEAGMTLGARKLKLGNLKLQEEGEASS 180
QY 652 TTSPTETQKLTVSHIEGYEQPIFLNVLAEIPGVVCAAGHNNQPSFAALLSSLNEL 711
Db 181 TTSPTETQKLTVSHIEGYEQPIFLNVLAEIPGVVCAAGHNNQPSFAALLSSLNEL 240
QY 712 GERQLVHVVKAKALPFRNLHVDDQMAVIOYSWGLMVFAMGWSRFTNVNSRMLYFAPD 771
Db 241 GERQLVHVVKAKALPFRNLHVDDQMAVIOYSWGLMVFAMGWSRFTNVNSRMLYFAPD 300
QY 772 LVFNEMRMKSRMYSQVCRMRHLSSQFGLWQITPQBFCKMALLFSIIPVDGLKNQKFF 831
Db 301 LVFNEMRMKSRMYSQVCRMRHLSSQFGLWQITPQBFCKMALLFSIIPVDGLKNQKFF 360
QY 832 DELRMNVIKELDRILACKRNKPTSCSRFFVOLTFLKLDVSQPIARELHQFTFDLLIKSHMV 891
Db 361 DELRMNVIKELDRILACKRNKPTSCSRFFVOLTFLKLDVSQPIARELHQFTFDLLIKSHMV 420
QY 892 SVDFPENMAELISVQVPKILSGKVKPIYFHTQ 923
Db 421 SVDFPENMAELISVQVPKILSGKVKPIYFHTQ 452

RESULT 12
AAG68238 standard; Protein; 839 AA.
XX ID AAG68238;
XX AC AAG68238;
XX DT 08-FEB-2002 (first entry)
XX DE Fused androgen receptor (AR) protein SEQ ID NO:11.
XX KW Human; androgen receptor; AR; fused androgen receptor protein;
XX KW fusion androgen receptor protein; sugar-combining protein;
XX KW maltose-combining protein.
XX OS Chimeric - Homo sapiens.
XX OS Chimeric - Unidentified.
XX PN JP2001252080-A.
XX PD 18-SEP-2001.
XX PF 13-MAR-2000; 2000JP-0069030.
XX PR 13-MAR-2000; 2000JP-0069030.
XX PA (TOYM) TOYOBO KK.
XX WPI: 2002-029658/04.
XX N-PSDB; ABA01683.
XX PT New polypeptide for screening drugs, comprises an androgen receptor
XX PT protein fused with a sugar-combining protein -
XX PS Claim 8; Page 11-13; 16pp; Japanese.
XX CC The present invention describes a fused androgen receptor (AR) protein
XX CC prepared by fusing an androgen receptor protein with a sugar-combining
XX CC protein. Also described are: (1) a gene encoding the above fused AR
XX CC protein; (2) a vector carrying the above gene; (3) a transformant in
XX CC which the above vector is introduced to a microbe and a gene encoding
XX CC the fused AR protein is expressed; (4) the preparation of a fused AR
XX CC protein in which the above transformant is cultured and the fused AR
XX CC protein is collected from the resultant culture; and (5) a reagent for
XX CC detecting the presence of interaction with a ligand containing the
XX CC above fused AR protein, a solvent for dissolving chemical substances
XX CC and a diluent liquid of the dissolved chemical substances. The fusion
XX CC protein can be used for screening drugs. The present sequence represents
XX CC the AR protein and sugar-combining protein fusion protein from the
XX CC present invention.
XX SQ Sequence 839 AA;
Query Match 48.9%; Score 2401; DB 23; Length 839;
Best Local Similarity 99.3%; Pred. No. 2e-153;
Matches 446; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 475 GGEAGAVPYGYTRPPQGLAGQESDFTAPDVWPGMVSRVYPSPPTCKSEMGPWMDSY 534
Db 391 GGEAGAVPYGYTRPPQGLAGQESDFTAPDVWPGMVSRVYPSPPTCKSEMGPWMDSY 450
QY 535 SGPGYDMRLTARDHVLPIIDYFPPOKTLICGDEASGCHYGALTCGSKVFFKRAAEGK 594
Db 451 SGPGYDMRLTARDHVLPIIDYFPPOKTLICGDEASGCHYGALTCGSKVFFKRAAEGK 510
QY 595 QKYLCAASNDCTIDKFRKNCPSRLKRCYEAGMTLGARKLKLGNLKLQEEGEASSTTS 654
Db 511 QKYLCAASNDCTIDKFRKNCPSRLKRCYEAGMTLGARKLKLGNLKLQEEGEASSTTS 570
QY 655 PTEETQKLTVSHIEGYEQPIFLNVLAEIPGVVCAAGHNNQPSFAALLSSLNELGER 714
Db 571 PTEETQKLTVSHIEGYEQPIFLNVLAEIPGVVCAAGHNNQPSFAALLSSLNELGER 630

QY 715 QLVHVYVWAKALPGFRNLHVDDQMAVIOYSWMGLMVFAMGWSFTNNSRMLYFAPDLVF 774
Db 631 QLVHVYVWAKALPGFRNLHVDDQMAVIOYSWMGLMVFAMGWSFTNNSRMLYFAPDLVF 690
QY 775 NEYRMHKSRYMSQCVRMHLSQEGWLOITPQEFCLMKALLLSIIPVDGLKNOKFFDEL 834
Db 691 NEYRMHKSRYMSQCVRMHLSQEGWLOITPQEFCLMKALLLSIIPVDGLKNOKFFDEL 750
QY 835 RMNYIKELDRIIACKRNPTSCSRFYQLTKLLDSVQPIARELHQFTFDLLIKSHMVSVD 894
Db 751 RMNYIKELDRIIACKRNPTSCSRFYQLTKLLDSVQPIARELHQFTFDLLIKSHMVSVD 810
QY 895 FPEMAEIIISVQVPKILSGVKPIYFHTQ 923
Db 811 FPEMAEIIISVQVPKILSGVKPIYFHTQ 839

RESULT 13
ABB83821
ID ABB83821 standard; Protein; 388 AA.
XX
AC ABB83821;
XX
DT 13-SEP-2002 (first entry)
XX
DE Human androgen receptor variant AR42 SEQ ID NO 2.
XX
KW Human; androgen receptor; receptor; AR: AR42; AR32; tumour; cancer;
KW steroid response element; prostate cancer; testis; gene therapy;
KW hormone therapy; cytostatic; contraceptive.
XX
OS Homo sapiens.
XX
PN EP1213300-A1.
XX
PD 12-JUN-2002.
XX
PE 26-OCT-2001; 2001EP-0250379.
XX
PR 30-NOV-2000; 2000DE-1061161.
XX
PA (SCHD) SCHERING AG.
XX
PI Ahrens-Fath I, Haendler B;
XX
DR WPI; 2002-530575/57.
XX
N-PSDB; ABB85656.
XX
PT New nucleic acid encoding variant forms of androgen receptor; useful
PT for diagnosis and treatment of prostatic cancer, also related proteins
PT and antibodies
XX
PS Claim 5; Page 9-11; 25pp; German.
XX
CC The invention relates to a nucleic acid (I) that encodes an androgen
CC receptor (AR) variant AR42 (ABB85656) or AR32 (ABB85657) or its
CC equivalents or a sequence that hybridises to them under stringent
CC conditions. Polypeptides (II, ABB83821-ABB83822) expressed by (I), can
CC bind androgens and other ligands and form heterodimers which can bind to
CC steroid response elements in target genes but do not induce activation,
CC so act as repressors of the known AR.(II) are used to raise specific
CC antibodies. (I) are used for recombinant production of (II) and as probes
CC for detecting (I)-related nucleic acid in tumour tissue. Also (I), (II),
CC a specific peptide and cells transfected with (I)-containing vectors, are
CC useful for identifying effectors of (II), specifically antiandrogenic
CC agents potentially useful for treating androgen-related diseases, e.g.
CC cancer of prostate or testis and as male contraceptives. (I) can be used
CC similarly in gene therapy. Antibodies to (II) are used to detect or
CC quantify (II) in tumour tissue, e.g. to determine if resistance to
CC hormone therapy is the result of altered expression of (II).
XX
SQ Sequence 388 AA;

Query Match 41.3%; Score 2029.5; DB 23; Length 388;
Best Local Similarity 97.2%; Pred. No. 8.7e-129;
Matches 383; Conservative 1; Mismatches 1; Indels 9; Gaps 1;
QY 530 WMSYSGPYGDMRLLETARDHVLPIIDYPPQKTCICGDEASGCHYGALTGSCSKVFFKR 589
Db 4 WLHS-----LETARDHVLPIIDYPPQKTCICGDEASGCHYGALTGSCSKVFFKR 54
QY 590 AAEQKQKYLCAARNDCITDKFRKKNPCSRRLKCYEAGMTLGARKLKLGNLKLQEEGEA 649
Db 55 AAEQKQKYLCAARNDCITDKFRKKNPCSRRLKCYEAGMTLGARKLKLGNLKLQEEGEA 114
QY 650 STTSPTTEETQKLTVSHIEGYECQPIFLNLEALEPVGVCAGHNNQPDGFAALLSSLN 709
Db 115 STTSPTTEETQKLTVSHIEGYECQPIFLNLEALEPVGVCAGHNNQPDGFAALLSSLN 174
QY 710 ELGERQLVHVYVWAKALPGFRNLHVDDQMAVIOYSWMGLMVFAMGWSFTNNSRMLYFA 769
Db 175 ELGERQLVHVYVWAKALPGFRNLHVDDQMAVIOYSWMGLMVFAMGWSFTNNSRMLYFA 234
QY 770 PDLVENEYRMHKSRYMSQCVRMHLSQEGWLOITPQEFCLMKALLLSIIPVDGLKNOK 829
Db 235 PDLVENEYRMHKSRYMSQCVRMHLSQEGWLOITPQEFCLMKALLLSIIPVDGLKNOK 294
QY 830 FDELRMNYIKELDRIIACKRNPTSCSRFYQLTKLLDSVQPIARELHQFTFDLLIKSH 889
Db 295 FDELRMNYIKELDRIIACKRNPTSCSRFYQLTKLLDSVQPIARELHQFTFDLLIKSH 354
QY 890 MVSVDPEMAEIIISVQVPKILSGVKPIYFHTQ 923
Db 355 MVSVDPEMAEIIISVQVPKILSGVKPIYFHTQ 388

RESULT 14
ABB83822
ID ABB83822 standard; Protein; 294 AA.
XX
AC ABB83822;
XX
DT 13-SEP-2002 (first entry)
XX
DE Human androgen receptor variant AR32 SEQ ID NO 4.
XX
KW Human; androgen receptor; receptor; AR: AR42; AR32; tumour; cancer;
KW steroid response element; prostate cancer; testis; gene therapy;
KW hormone therapy; cytostatic; contraceptive.
XX
OS Homo sapiens.
XX
PN EP1213300-A1.
XX
PD 12-JUN-2002.
XX
PE 26-OCT-2001; 2001EP-0250379.
XX
PR 30-NOV-2000; 2000DE-1061161.
XX
PA (SCHD) SCHERING AG.
XX
PI Ahrens-Fath I, Haendler B;
XX
DR WPI; 2002-530575/57.
XX
N-PSDB; ABB85657.
XX
PT New nucleic acid encoding variant forms of androgen receptor; useful
PT for diagnosis and treatment of prostatic cancer, also related proteins
PT and antibodies
XX
PS Claim 5; Page 11-12; 25pp; German.
XX
CC The invention relates to a nucleic acid (I) that encodes an androgen
CC receptor (AR) variant AR42 (ABB85656) or AR32 (ABB85657) or its

CC equivalents or a sequence that hybridises to them under stringent
CC conditions. Polypeptides (II, ABB83821-ABB83822) expressed by (I), can
CC bind androgens and other ligands and form heterodimers which can bind to
CC steroid response elements in target genes but do not induce activation,
CC so act as repressors of the known AR. (II) are used to raise specific
CC antibodies. (I) are used for recombinant production of (II) and as probes
CC for detecting (I)-related nucleic acid in tumour tissue. Also (I), (II),
CC a specific peptide and cells transfected with (I)-containing vectors, are
CC useful for identifying effectors of (II), specifically antiandrogenic
CC agents potentially useful for treating androgen-related diseases, e.g.
CC cancer of prostate or testis and as male contraceptive. (I) can be used
CC similarly in gene therapy. Antibodies to (II) are used to detect or
CC quantify (II) in tumour tissue, e.g. to determine if resistance to
CC hormone therapy is the result of altered expression of (II).

XX SQ Sequence 294 AA;
Query Match 30.4%; Score 1493.5; DB 23; Length 294;
Best Local Similarity 100.0%; Pred. No. 9e-93;
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 543 LETARDHVLPIIDYFPQKTLICGDEASGCHYGALTGCGSKVFFKRAAEKGKQKYLCSAR 602
DB 8 LETARDHVLPIIDYFPQKTLICGDEASGCHYGALTGCGSKVFFKRAAEKGKQKYLCSAR 67
QY 603 NDCITIDFRKNCPSCELRKCYEAGMTLGARKLKLGKLNKLOEGEASGTSPTETTTOK 662
DB 68 NDCITIDFRKNCPSCELRKCYEAGMTLGARKLKLGKLNKLOEGEASGTSPTETTTOK 127
QY 663 LTVSHIEGYECOPTIFLNLVLEAIEPGVVCAGHDNNQPDFAALLSSLNELGERQLVHVVKW 722
DB 128 LTVSHIEGYECOPTIFLNLVLEAIEPGVVCAGHDNNQPDFAALLSSLNELGERQLVHVVKW 187
QY 723 AKALPGFRNLHVDQMAVIOYSWMGLMVFAMGWRSTNNVNSRMLYFAPDLVFNEMRHS 782
DB 188 AKALPGFRNLHVDQMAVIOYSWMGLMVFAMGWRSTNNVNSRMLYFAPDLVFNEMRHS 247
QY 793 RMYSOCVRMRHLSQEFGLQITPOEFLCMKALLFSI 819
DB 248 RMYSOCVRMRHLSQEFGLQITPOEFLCMKALLFSI 284

RESULT 15
AAR12230
ID AAR12230 standard; Protein; 630 AA.
XX AC AAR12230;
XX DT 20-AUG-1991 (first entry)
XX DE TrpE/androgen receptor DNA-binding domain fusion protein.
XX KW androgen receptor; AR; DNA-binding protein; steroid hormone.
XX OS Homo sapiens.
XX FH Key
XX FT Protein
XX FT Location/Qualifiers
XX FT 1..323
XX FT /label= 33kD trpE protein
XX FT 324..334
XX FT /label= 11 amino acid linker
XX FT 335..613
XX FT /label= 29kD protein incl. AR DNA-binding domain
XX FT 614..630
XX FT /label= 17 amino acid linker
XX PN WO9107423-A.
XX 30-MAY-1991.
XX PD 19-OCT-1990; 90WO-US06015.
XX PF 17-NOV-1989; 89US-0438775.
XX PR

XX (ARCH-) ARCH DEV CORP.
XX PA Liao S, Chang C;
XX PI WPI; 1991-178048/24.
XX DR N-PSDB; AAQ12008.
XX DR Androgen receptor and TR2 DNA binding proteins - DNA sequences
XX PT and antibodies for detection and quantification methods
XX PS Example 13; Fig 10; 79pp; English.
XX To express an androgen receptor fusion protein in E.coli, the PATH
XX expression system was used. The trpE is insoluble so partially
XX purified induced fusion protein is obtained by simply lysing the
XX E.coli and precipitating the insoluble fusion protein. The fusion
XX protein was used for immunisation to obtain monoclonal anti-AR
XX antibodies.
XX SQ Sequence 630 AA;
Query Match 29.7%; Score 1459; DB 12; Length 630;
Best Local Similarity 79.9%; Pred. No. 5.1e-90;
Matches 286; Conservative 17; Mismatches 31; Indels 24; Gaps 6;
QY 515 VYPSPPTCV-----KSEMGPM-----DS-----YSGPYGDMRLE-TARDHVLPIIDYFPP 559
DB 272 LPCPSPLAAVYVLLKSNPSYPMFFMQDNDFTLFGASPESSLYDATSRQIFIPGRARIRA 331
QY 560 QKTCILCGDEASGCHYGALTGCGSKVFFKRAAEKGKQKYLCSARNDCTIDKFRKNCPSCR 619
DB 332 RPG--ICGDEASGCHYGALTGCGSKVFFKRAAEKGKQKYLCSARNDCTIDKFRKNCPSCR 389
QY 620 LRKYEAGMTLGARKLKLGKLNKLOEGEASGTSPTETTTOKLTVSHIEGYECOPTIFLN 679
DB 390 LRKYEAGMTLGARKLKLGKLNKLOEGEASGTSPTETTTOKLTVSHIEGYECOPTIFLN 449
QY 680 VLEAIEPGVVCAGHDNNQPDFAALLSSLNELGERQLVHVVKWAKALPGFRNLHVDQMA 739
DB 450 VLEAIEPGVVCAGHDNNQPDFAALLSSLNELGERQLVHVVKWAKALPGFRNLHVDQMA 509
QY 740 VIOYSWMGLMVFAMGWRSTNNVNSRMLYFAPDLVFNEMRHSRMYSOCVRMRHLSQEF 799
DB 510 VIOYSWMGLMVFAMGWRSTNNVNSRMLYFAPDLVFNEMRHSRMYSOCVRMRHLSQEF 569
QY 800 WLQITPOEFLCMKALLFSIIPVDGLKNOKFFDELRMNVIKELDRIIACKRKNPTSCS 857
DB 570 WLQITPOEFLCMKALLFSIIPVDGLKNOKFFDELRMNVIKELDRIIACKRKNPTSCS 620

Search completed: April 28, 2003, 13:50:40
Job time : 49 secs